SEQUENCE LISTING

<110> Debinski, Waldemar
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<120> IL13 MUTANTS

<130> 6460-28

<140> US 09/679,710
<141> 2000-10-05

<160> 23

<170> PatentIn version 3.0

<210> 1
<211> 114
<212> PRT
<213> Homo sapiens

<400> 1

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
      20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
    35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
 50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
      85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
      100   105   110

Phe Asn

<210> 2
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220> .
<221> misc_feature
<223> hIL13 mutant having a Glu to Lys substitution at residue 13

<400> 2

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Lys Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
            20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
        35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
        50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
            85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
            100   105   110

Phe Asn

<210> 3
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Glu to Ile substitution at residue 13

<400> 3

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Ile Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
        20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
        35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
        50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
                85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
            100   105   110

Phe Asn

<210> 4
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Glu to Cys substitution at residue 13

<400> 4

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Cys Leu Ile Glu

```
       1          5           10          15
```

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
```
            20          25          30
```

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
```
            35          40          45
```

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
```
          50          55          60
```

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
```
     65          70          75          80
```

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
```
               85          90          95
```

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
```
          100         105         110
```

Phe Asn

<210> 5
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Glu to Ser substitution at residue 13

<400> 5

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Ser Leu Ile Glu
```
1          5           10          15
```

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
```
          20          25          30
```

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
```
     35          40          45
```

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
          85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
          100   105   110

Phe Asn

<210> 6
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Glu to Arg substitution at residue 13

<400> 6

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Arg Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
          20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
          35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
          85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
      100   105   ·110

Phe Asn

<210> 7
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Glu to Tyr substitution at residue 13

<400> 7

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Tyr Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
      20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
    35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
  50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70 ·   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
      85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
      100   105   110

Phe Asn

<210> 8

<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Glu to Asp substitution at residue 13

<400> 8

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Asp Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
        20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
        35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
    50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
        85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
        100   105   110

Phe Asn

<210> 9
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Glu to Lys substitution at residue 16

<400> 9

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Lys
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
            20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
        35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
    50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
            85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
            100   105   110

Phe Asn

<210> 10
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Glu to Lys substitution at residue 17

<400> 10

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Lys Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
            20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
    35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
    50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
      85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
      100   105   110

Phe Asn

<210> 11
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Arg to Asp substitution at residue 66

<400> 11

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
    20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
    35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
    50   55   60

Gln Asp Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln

```
        65          70          75          80
```

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
```
            85          90          95
```

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
```
            100         105         110
```

Phe Asn

<210> 12
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Ser to Asp substitution at residue 69

<400> 12

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
```
1           5           10          15
```

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
```
            20          25          30
```

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
```
            35          40          45
```

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
```
            50          55          60
```

Gln Arg Met Leu Asp Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
```
65          70          75          80
```

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
```
            85          90          95
```

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
```
            100         105         110
```

Phe Asn

<210> 13
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Asp to Lys substitution at residue 99

<400> 13

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
            20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
        35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
        50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
                85   90   95

Val Lys Lys Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
                100   105   110

Phe Asn

<210> 14
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Leu to Ala substitution at residue 102

<400> 14

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
                20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
            35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
        50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
            85   90   95

Val Lys Asp Leu Leu Ala His Leu Lys Lys Leu Phe Arg Glu Gly Arg
            100   105   110

Phe Asn

<210> 15
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Leu to Ala substitution at residue 104

<400> 15

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu

```
1        5           10          15
```

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
```
        20          25          30
```

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
```
        35          40          45
```

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
```
    50          55          60
```

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
```
65          70          75          80
```

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
```
            85          90          95
```

Val Lys Asp Leu Leu Leu His Ala Lys Lys Leu Phe Arg Glu Gly Arg
```
            100         105         110
```

Phe Asn

<210> 16
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Lys to Asp substitution at residue 105

<400> 16

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
```
1        5           10          15
```

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
```
        20          25          30
```

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
```
        35          40          45
```

```
Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
     50              55              60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
 65          70              75              80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
             85              90              95

Val Lys Asp Leu Leu Leu His Leu Asp Lys Leu Phe Arg Glu Gly Arg
             100             105             110

Phe Asn
```

<210> 17
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Lys to Asp substitution at residue 106

<400> 17

```
Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1           5               10              15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
         20              25              30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
     35              40              45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
     50              55              60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
 65          70              75              80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
             85              90              95
```

Val Lys Asp Leu Leu Leu His Leu Lys Asp Leu Phe Arg Glu Gly Arg
      100   105   110

Phe Asn

<210> 18
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Leu to Ala substitution at residue 107

<400> 18

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
     20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
    35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
  50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
      85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Ala Phe Arg Glu Gly Arg
      100   105   110

Phe Asn

<210> 19

<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Phe to Tyr substitution at residue 108

<400> 19

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
            20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
        35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
    50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
            85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Tyr Arg Glu Gly Arg
        100   105   110

Phe Asn

<210> 20
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Arg to Asp substitution at residue 109

<400> 20

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
            20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
            35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
            50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
                85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Asp Glu Gly Arg
                100   105   110

Phe Asn

<210> 21
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Arg to Asp substitution at residue 112

<400> 21

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
            20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
    35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
   50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
            85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Asp
        100   105   110

Phe Asn

<210> 22
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having a Phe to Asp substitution at residue 113

<400> 22

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
        20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
    35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
   50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln

65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
            85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
            100   105   110

Asp Asn

<210> 23
<211> 114
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<221> misc_feature
<223> hIL13 mutant having an Asn to Asp substitution at residue 113

<400> 23

Ser Pro Gly Pro Val Pro Pro Ser Thr Ala Leu Arg Glu Leu Ile Glu
1   5   10   15

Glu Leu Val Asn Ile Thr Gln Asn Gln Lys Ala Pro Leu Cys Asn Gly
            20   25   30

Ser Met Val Trp Ser Ile Asn Leu Thr Ala Gly Met Tyr Cys Ala Ala
            35   40   45

Leu Glu Ser Leu Ile Asn Val Ser Gly Cys Ser Ala Ile Glu Lys Thr
            50   55   60

Gln Arg Met Leu Ser Gly Phe Cys Pro His Lys Val Ser Ala Gly Gln
65   70   75   80

Phe Ser Ser Leu His Val Arg Asp Thr Lys Ile Glu Val Ala Gln Phe
            85   90   95

Val Lys Asp Leu Leu Leu His Leu Lys Lys Leu Phe Arg Glu Gly Arg
            100   105   110

Phe Asp